We claim

1. A method for increasing cellulose biosynthesis in cotton plants, comprising the step of:
providing cells of said cotton plant with a chimeric gene comprising the following operably linked DNA fragments
i) a promoter expressible in said cell of said plant;
ii) a DNA region coding for the protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8 or a variant thereof, said variant having the same enzymatic activity;
iii) a 3' region involved in transcription termination and polyadenylation;
thereby increasing cellulose biosynthesis in said plant.

2. The method of claim 1, wherein said DNA region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 121 to the nucleotide at position 1986, or SEQ ID No. 2 from the nucleotide at position 47 to the nucleotide at position 1906, or SEQ ID No 3 or SEQ ID No 4 from the nucleotide at position 2 to the nucleotide at position 1576, or SEQ ID No. 9.

3. The method of claim 1, wherein said promoter is a constitutive promoter.

4. The method of claim 1, wherein said promoter is a fiber-specific promoter.

5. The method of claim 1, wherein said promoter is an expansin promoter.

6. The method of claim 1, wherein said cellulose biosynthesis is increased in lint fibers.

7. A method for decreasing cellulose biosynthesis in cotton plants comprising the step of:
providing cells of said cotton plant with a chimeric gene capable of reducing the expression of a gene endogenous to said cotton plant, wherein said endogenous gene codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8

thereby decreasing cellulose biosynthesis.

8. The method of claim 7, wherein said chimeric gene comprises

21 contiguous nucleotides selected from a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No 6 or SEQ ID No 7 or SEQ ID No 8,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

9. The method of claim 8, wherein said 21 contiguous nucleotides are selected from the nucleotide sequence of SEQ ID No 1 or SEQ ID No. 2 or SEQ ID No 3 or SEQ ID No 4 or SEQ ID No. 9.

10. The method of claim 7, wherein said chimeric gene comprises

21 contiguous nucleotides selected from the complement of a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

11. The method of claim 10, wherein said 21 contiguous nucleotides are selected from the complement of the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4 or SEQ ID No. 9.

12. The method of claim 7, wherein said chimeric gene comprises

a first nucleotide sequence of 21 contiguous nucleotides selected from a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 5 or SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8, and

a second nucleotide sequence complementary to said first nucleotide sequence,

operably linked to a plant-expressible promoter and a 3' region involved in transcription termination and polyadenylation

such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

13. The method of claim 12, wherein said 21 contiguous nucleotides are selected from the nucleotide sequence of SEQ ID No. 1 or SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4 or SEQ ID No. 9.

14. The method of claim 7, wherein said plant expressible promoter is a constitutive promoter.

15. The method of claim 7, wherein said plant expressible promoter is a fuzz fiber specific promoter.

16 . The method of claim 7, wherein said cellulose biosynthesis is decreased in fuzz fiber production.

17 . A chimeric gene comprising the following operably linked DNA fragments:

i) a promoter expressible in plant cells;

ii) a DNA region coding for a protein comprising the amino acid sequence of SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8; and

iii) a 3'end region involved in transcription termination and polyadenylation.

18. The chimeric gene of claim 17, wherein said DNA region comprises the nucleotide sequence of SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4.

19 . The chimeric gene of claim 17, wherein said promoter is a constitutive promoter.

20 . The chimeric gene of claim 17, wherein said promoter is a fiber-specific promoter.

21 . The chimeric gene of claim 17, wherein said promoter is an expansin promoter.

22 . A plant cell comprising the chimeric gene of claim 17.

23. A plant comprising a plant cell according to claim 22.

24. A seed of the plant of claim 23.

25. A chimeric gene comprising

a first nucleotide sequence of 21 contiguous nucleotides selected from a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8,

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

26. A chimeric gene according to claim 25, further comprising a second nucleotide sequence complementary to said first nucleotide sequence, operably linked to said first nucleotide sequence such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

27. A chimeric gene according to claim 25, wherein said first sequence of 21 contiguous nucleotides is selected from the nucleotide sequence of SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4.

28. A chimeric gene according to claim 27, further comprising a second nucleotide sequence complementary to said first nucleotide sequence, operably linked to said first nucleotide sequence such that upon transcription of said chimeric gene, an RNA is formed which can form a double stranded RNA region between said first and said second nucleotide sequence.

29. A plant cell comprising the chimeric gene of claim 25

30. A plant comprising a plant cell according to claim 29.

31. A seed of the plant of claim 30.

32. A chimeric gene comprising

a first nucleotide sequence of 21 contiguous nucleotides selected from the complement of a nucleotide sequence which codes for a protein comprising the amino acid sequence of SEQ ID No. 6 or SEQ ID No. 7 or SEQ ID No. 8

operably linked to a plant expressible promoter and a 3' region involved in transcription termination and polyadenylation.

33. A chimeric gene according to claim 32, wherein said first nucleotide sequence of 21 contiguous nucleotides is selected from the complement of the nucleotide sequence of SEQ ID No. 2 or SEQ ID No. 3 or SEQ ID No. 4.

34. A chimeric gene according to claim 32, wherein said plant expressible promoter is a constitutive promoter.

35. A chimeric gene according to claim 32, wherein said plant expressible promoter is a fuzz fiber specific promoter.

36. A plant cell comprising the chimeric gene of claim 32.

37. A plant comprising a plant cell according to claim 36.

38. A seed of the plant of claim 37.

39. A method for identifying allelic variations of the genes encoding proteins involved in cellulose biosynthesis in a population of different genotypes or varieties of a fiber producing plant species, which are correlated either alone or in combination with the quantity and/or quality of cellulose production, and fiber production comprising the steps of:

a) providing a population of different varieties or genotypes of a particular plant species or interbreeding plant species comprising different allelic forms of the nucleotide sequences encoding proteins comprising the amino acid sequences of SEQ ID No. 5, 6, 7 or 8;

b) determining parameters related to fiber production and/or cellulose biosynthesis or each individual of the population;

c) determining the presence of a particular allelic form of the nucleotide sequences encoding proteins comprising the amino acid sequences of SEQ ID No. 5, 6, 7 or 8 for each individual of the population; and

d) correlating the occurrence of particular fiber or cellulose parameters with the presence of a particular allelic form of the mentioned nucleotide sequence or a particular combination of such allelic forms;

and thereby identifying said allelic variations.